ATGAGCTATTACGGAAGTAGCTACCGGATTGTCAATGTGGACTCCAAATATCCAGGCTATCCTCC AGAGCATGCCATCGCTGAGAAGAGAGAGCCAAGAAGGCGCTTGCTCCACAAAGATGGCAGCTGTA ATGTGTACTTTAAACACATTTTTGGAGAATGGGGGAGCTACATGGTTGATATTTTTACCACTCTT GTGGATACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCTTACATTCTCTCTGGTTGAT ATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCACGGAGACCTATTAAGCGATCCAGATATCA CCCCTTGTGTTGACAACGTGCATTCATTTACGGCTGCATTTTTATTCTCCCTGGAGACCCAGACC ACCATTGGATACGGTTACCGCTGTGTCACCGAAGAGTGCTCTGTGGCTGTACTGACAGTGATCCT TCAGTCCATCCTCAGCTGCATCATAAACACCTTCATCATTGGAGCAGCCTTGGCAAAGATGGCAA CTGCCCGGAAGAGCCCAGACCATACGCTTCAGCTATTTTGCCCTCATTGGTATGAGAGACGGG AAGCCTTGCCTCATGTGGCGCATAGGTGACTTCCGACCAAACCATGTGGTAGAGGGCACGGTGAG AGCCCAACTTCTGCGCTATTCAGAAGACAGTGAAGGGAGGATGACGATGGCGTTTAAAGACCTCA AACTCGTCAATGACCAGATAATCCTGGTAACTCCAGTGACTATTGTCCATGAAATTGACCATGAG AGCCCTCTGTATGCCCTTGACCGCAAGGCAGTGGCCAAAGATAATTTCGAGATTCTGGTGACATT TATTTATACTGGTGATTCCACTGGGACATCCCACCAGTCCAGAAGTTCCTACATCCCCAGAGAAA TTCTCTGGGGCCACAGGTTTCATGATGTATTGGAAGTGAAGAGAAAGTACTACAAGGTGAACTGC TTGCAGTTTGAAGGAAGCGTGGAAGTCTACGCCCCCTTTTTGCAGTGCCAAACAACTGGACTGGAA GGACCAACAACTCAACAACTTGGAGAAAACGTCCCCTGCCCGAGGATCCTGCAATTCTGACACCA ACACCAGGAGGCGGTCCTTCAGCGCAGTTGCCGTGGTGAGCAGCTGTGAGAACCCAGAGGAGACC GTCCTGTCCCCACAAGATGAATGTAAGGAGATGCCCTATCAGAAAGCCCTCCTGACTTTAAATAG GATCTCCATGGAATCCCAGATG (SEQ ID NO:1)

MSYYGSSYRIVNVDSKYPGYPPEHAIAEKRRARRRLLHKDGSCNVYFKHIFGEWGSYMVDIFTT LVDTKWRHMFIIFSLSYILSWLIFGSIFWLIAFHHGDLLSDPDITPCVDNVHSFTAAFLFSLET QTTIGYGYRCVTEECSVAVLTVILQSILSCIINTFIIGAALAKMATARKRAQTIRFSYFALIGM RDGKPCLMWRIGDFRPNHVVEGTVRAQLLRYSEDSEGRMTMAFKDLKLVNDQIILVTPVTIVHE IDHESPLYALDRKAVAKDNFEILVTFIYTGDSTGTSHQSRSSYIPREILWGHRFHDVLEVKRKY YKVNCLQFEGSVEVYAPFCSAKQLDWKDQQLNNLEKTSPARGSCNSDTNTRRRSFSAVAVVSSC ENPEETVLSPQDECKEMPYQKALLTLNRISMESQM (SEQ ID NO:2)

<u>underlined</u> = deleted in targeting construct

**BOLD** = sequence flanking Neo insert in targeting construct

ATGAGCTATTACGGAAGTAGCTACCGGATTGTCAATGTGGACTCCAAATATCCAGGCTAT CCTCCAGAGCATGCCATCGCTGAGAAGAGAAGAGCAAGAAGGCGCTTGCTCCACAAAGAT GGCAGCTGTAATGTGTACTTTAAACACATTTTTTGGAGAATGGGGGAGCTACATGGTTGAT ATTTTTACCACTCTTGTGGATACCAAGTGGCGCCATATGTTCATAATATTTTCTCTGTCT TACATTCTCTCCTGGTTGATATTTGGTTCCATATTTTGGCTCATAGCCTTTCATCACGGA GAAGAGTGCTCTGTGGCTGTACTGACAGTGATCCTTCAGTCCATCCTCAGCTGCATCATA AACACCTTCATCATTGGAGCAGCCTTGGCAAAGATGGCAACTGCCCGGAAGAGAGCCCAG ACCATACGCTTCAGCTATTTTGCCCTCATTGGTATGAGAGACGGGAAGCCTTGCCTCATG TGGCGCATAGGTGACTTCCGACCAAACCATGTGGTAGAGGGCACGGTGAGAGCCCAACTT CTGCGCTATTCAGAAGACAGTGAAGGGAGGATGACGATGGCGTTTAAAGACCTCAAACTC GTCAATGACCAGATAATCCTGGTAACTCCAGTGACTATTGTCCATGAAATTGACCATGAG AGCCCTCTGTATGCCCTTGACCGCAAGGCAGTGGCCAAAGATAATTTCGAGATTCTGGTG **ACATTTATTTATACTGGTGATTCCAC**TGGGACATCCCACCAGTCCAGAAGTTCCTACATC CCCAGAGAAATTCTCTGGGGCCACAGGTTTCATGATGTATTGGAAGTGAAGAGAAAGTAC TACAAGGTGAACTGCTTGCAGTTTGAAGGAAGCGTGGAAGTCTACGCCCCCTTTTGCAGT GCCAAACAACTGGACTGGAAGGACCAACAACTCAACAACTTGGAGAAAACGTCCCCTGCC CGAGGATCCTGCAATTCTGACACCAACACCAGGAGGCGGTCCTTCAGCGCAGTTGCCGTG GTGAGCAGCTGTGAGAACCCAGAGGAGACCGTCCTGTCCCCACAAGATGAATGTAAGGAG ATGCCCTATCAGAAAGCCCTCCTGACTTTAAATAGGATCTCCATGGAATCCCAGATG

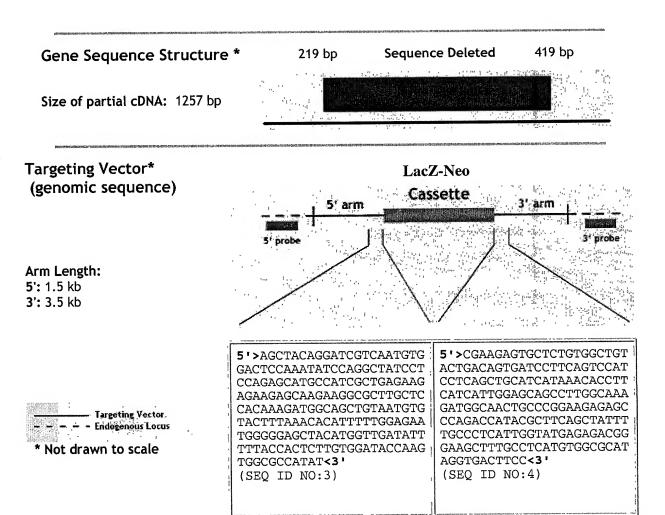


FIGURE 4

4 h .

	PP090P110	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	PP100P120	218.6	702.1	207.1	181.6	188.5	348.3	122.0	175.8	272.6	168.0	282.7	832.1	97.3	76.2	42.9	279.7	325.2	66.8	180.7
	PP090P120	544.4	1282.2	716.4	463.8	482.4	1268.4	437.6	902.8	823.3	701.6	929.2	1543.1	180.7	114.2	104.5	1194.8	930.1	151.0	791.3
	PP085P120	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	PP080P120	1927.8	1476.6	2036.3	1534.7	813.4	2639.2	1670.8	1794.9	1256.9	1429.2	1745.7	2379.4	473.4	393.1	350.7	1677.8	1712.9	295.4	861.8
	P120	2315.9	1883.7	2493.1	2250.3	969.3	2369.6	1674.3	1800.2	1807.1	1469.2	1577.7	2686.0	641.1	308.5	466.8	1992.7	1738.3	291.0	1312.0
	P110	1821.2	1154.4	1751.5	1495.0	446.7	1840.5	1367.7	1088.9	1753.9	7.976	1173.8	2023.0	9.819	229.5	348.6	1420.5	538.5	370.6	614.4
	P100	1198.3	403.3	458.9	381.4	140.6	450.7	439.5	378.5	671.4	115.2	486.3	284.6	334.5	106.0	45.8	497.5	78.6	118.2	70.7
	P090	343.7	42.4	55.0	79.1	54.1	98.1	9.76	112.3	163.1	38.9	25.1	24.1	70.2	37.0	19.7	31.7	34.6	9.09	38.0
	P085	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	P080	20.6	19.8	22.6	50.3	45.4	23.8	27.8	34.2	35.2	62.5	19.7	21.3	27.0	40.5	16.5	23.7	49.8	142.9	28.2
Average Highest Voltage (volts)	No Stimulation	30.8	16.8	19.7	35.8	30.3	20.6	37.5	42.4	23.7	51.1	16.4	23.2	21.7	31.2	25.6	24.6	48.7	70.8	42.4
	Age (Days)	9/	77	77	78	77	11	77	73	73	78	9/	77	78	77	11	11	11	73	73
	Genotype	-/-	-/-	<i>\</i>	+	-/-	-/-	-/-	-/-	-/-	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+	+/+